RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/824,134

DATE: 06/26/2001
TIME: 15:11:31

Input Set : N:\Crf3\RULE60\09824134.txt
Output Set: N:\CRF3\06262001\I824134.raw

SEQUENCE LISTING

ENTERED

```
 4 (1) GENERAL INFORMATION:
 6        (i) APPLICANT: WALLACH, David
 7                      BOLDIN, Mark
 8                      VARFOLOMEEV, Eugene
 9                      METT, Igor
11       (ii) TITLE OF INVENTION: MODULATORS OF THE FUNCTION OF FAS/APO1
12                                RECEPTORS
14      (iii) NUMBER OF SEQUENCES: 2
16       (iv) CORRESPONDENCE ADDRESS:
17            (A) ADDRESSEE: BROWDY AND NEIMARK, P.L.L.C.
18            (B) STREET: 419 Seventh Street N.W., Ste. 300
19            (C) CITY: Washington
20            (D) STATE: D.C.
21            (E) COUNTRY: United States of America
22            (F) ZIP: 20004
24        (v) COMPUTER READABLE FORM:
25            (A) MEDIUM TYPE: Floppy disk
26            (B) COMPUTER: IBM PC compatible
27            (C) OPERATING SYSTEM: PC-DOS/MS-DOS
28            (D) SOFTWARE: PatentIn Release #1.0, Version #1.30
30       (vi) CURRENT APPLICATION DATA:
C--> 31       (A) APPLICATION NUMBER: US/09/824,134
C--> 32       (B) FILING DATE: 03-Apr-2001
46      (vii) PRIOR APPLICATION DATA:
35            (A) APPLICATION NUMBER: 08/860,082
36            (B) FILING DATE:
39            (A) APPLICATION NUMBER: IL 112022
40            (B) FILING DATE: 15-DEC-1994
43            (A) APPLICATION NUMBER: IL 112692
44            (B) FILING DATE: 19-FEB-1995
47            (A) APPLICATION NUMBER: IL 114615
48            (B) FILING DATE: 16-JUL-1995
50     (viii) ATTORNEY/AGENT INFORMATION:
51            (A) NAME: BROWDY, Roger L.
52            (B) REGISTRATION NUMBER: 25,618
53            (C) REFERENCE/DOCKET NUMBER: WALLACH=16
55       (ix) TELECOMMUNICATION INFORMATION:
56            (A) TELEPHONE: (202) 628-5197
57            (B) TELEFAX: (202) 737-3528
60 (2) INFORMATION FOR SEQ ID NO: 1:
62        (i) SEQUENCE CHARACTERISTICS:
63            (A) LENGTH: 1701 base pairs
64            (B) TYPE: nucleic acid
65            (C) STRANDEDNESS: single
66            (D) TOPOLOGY: linear
68       (ii) MOLECULE TYPE: cDNA
```

RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/824,134

Input Set : N:\Crf3\RULE60\09824134.txt
Output Set: N:\CRF3\06262001\I824134.raw

```
70      (ix) FEATURE:
71           (A) NAME/KEY: CDS
72           (B) LOCATION: 1..768
74      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:
76 GTG AAT CAG GCA CCG GAG TGC AGG TTC GGG GGT GGA ATC CTT GGG CCG       48
77 Val Asn Gln Ala Pro Glu Cys Arg Phe Gly Gly Gly Ile Leu Gly Pro
78  1               5                  10                  15
80 CTG GGC AAG CGG CGA GAC CTG GCC AGG GCC AGC GAG CCG AGG ACA GAG       96
81 Leu Gly Lys Arg Arg Asp Leu Ala Arg Ala Ser Glu Pro Arg Thr Glu
82              20                  25                  30 .
84 GGC GCG CGG AGG GCC GGG CCG CAG CCC CGG CCG CTT GCA GAC CCC GCC      144
85 Gly Ala Arg Arg Ala Gly Pro Gln Pro Arg Pro Leu Ala Asp Pro Ala
86              35                  40                  45
88 ATG GAC CCG TTC CTG GTG CTG CTG CAC TCG GTG TCG TCC AGC CTG TCG      192
89 Met Asp Pro Phe Leu Val Leu Leu His Ser Val Ser Ser Ser Leu Ser
90         50                  55                  60
92 AGC AGC GAG CTG ACC GAG CTC AAG TTC CTA TGC CTC GGG CGC GTG GTC      240
93 Ser Ser Glu Leu Thr Glu Leu Lys Phe Leu Cys Leu Gly Arg Val Val
94 65                  70                  75                  80
96 AAG CGC AAG CTG GAG CGC GTG CAG AGC GGC CTA GAC CTC TTC TCC ATG      288
97 Lys Arg Lys Leu Glu Arg Val Gln Ser Gly Leu Asp Leu Phe Ser Met
98                  85                  90                  95
100 CTG CTG GAG CAG AAC GAC CTG GAG CCC GGG CAC ACC GAG CTC CTG CGC     336
101 Leu Leu Glu Gln Asn Asp Leu Glu Pro Gly His Thr Glu Leu Leu Arg
102                 100                 105                 110
104 GAG CTG CTC GCC TCC CTG CGG CGC CAC GAC CTG CTG CGG CGC GTC GAC     384
105 Glu Leu Leu Ala Ser Leu Arg Arg His Asp Leu Leu Arg Arg Val Asp
106             115                 120                 125
108 GAC TTC GAG GCG GGG GCG GCG GCC GGG GCC GCG CCT GGG GAA GAA GAC     ·432
109 Asp Phe Glu Ala Gly Ala Ala Ala Gly Ala Ala Pro Gly Glu Glu Asp
110         130                 135                 140
112 CTG TGT GCA GCA TTT AAC GTC ATA TGT GAT AAT GTG GGG AAA GAT TGG     480
113 Leu Cys Ala Ala Phe Asn Val Ile Cys Asp Asn Val Gly Lys Asp Trp
114 145                 150                 155                 160
116 AGA AGG CTG GCT CGT CAG CTC AAA GTC TCA GAC ACC AAG ATC GAC AGC     528
117 Arg Arg Leu Ala Arg Gln Leu Lys Val Ser Asp Thr Lys Ile Asp Ser
118                 165                 170                 175
120 ATC GAG GAC AGA TAC CCC CGC AAC CTG ACA GAG CGT GTG CGG GAG TCA     576
121 Ile Glu Asp Arg Tyr Pro Arg Asn Leu Thr Glu Arg Val Arg Glu Ser
122                 180                 185                 190
124 CTG AGA ATC TGG AAG AAC ACA GAG AAG GAG AAC GCA ACA GTG GCC CAC     624
125 Leu Arg Ile Trp Lys Asn Thr Glu Lys Glu Asn Ala Thr Val Ala His
126             195                 200                 205
128 CTG GTG GGG GCT CTC AGG TCC TGC CAG ATG AAC CTG GTG GCT GAC CTG     672
129 Leu Val Gly Ala Leu Arg Ser Cys Gln Met Asn Leu Val Ala Asp Leu
130         210                 215                 220
132 GTA CAA GAG GTT CAG CAG GCC CGT GAC CTC CAG AAC AGG AGT GGG GCC     720
133 Val Gln Glu Val Gln Gln Ala Arg Asp Leu Gln Asn Arg Ser Gly Ala
134 225                 230                 235                 240
```

```
136 ATG TCC CCG ATG TCA TGG AAC TCA GAC GCA TCT ACC TCC GAA GCG TCC          768
137 Met Ser Pro Met Ser Trp Asn Ser Asp Ala Ser Thr Ser Glu Ala Ser
138              245                  250                  255
140 TGATGGGCCG CTGCTTTGCG CTGGTGGACC ACAGGCATCT ACACAGCCTG GACTTTGGTT          828
142 CTCTCCAGGA AGGTAGCCCA GCACTGTGAA GACCCAGCAG GAAGCCAGGC TGAGTGAGCC          888
144 ACAGACCACC TGCTTCTGAA CTCAAGCTGC GTTTATTAAT GCCTCTCCCG CACCAGGCCG          948
146 GGCTTGGGCC CTGCACAGAT ATTTCCATTT CTTCCTCACT ATGACACTGA GCAAGATCTT         1008
148 GTCTCCACTA AATGAGCTCC TGCGGGAGTA GTTGGAAAGT TGGAACCGTG TCCAGCACAG         1068
150 AAGGAATCTG TGCAGATGAG CAGTCACACT GTTACTCCAC AGCGGAGGAG ACCAGCTCAG         1128
152 AGGCCCAGGA ATCGGAGCGA AGCAGAGAGG TGGAGAACTG GGATTTGAAC CCCCGCCATC         1188
154 CTTCACCAGA GCCCATGCTC AACCACTGTG GCGTTCTGCT GCCCCTGCAG TTGGCAGAAA         1248
156 GGATGTTTTT GTCCCATTTC CTTGGAGGCC ACCGGGACAG ACCTGGACAC TAGGGTCAGG         1308
158 CGGGGTGCTG TGGTGGGGAG AGGCATGGCT GGGGTGGGGG TGGGGAGACC TGGTTGGCCG         1368
160 TGGTCCAGCT CTTGGCCCCT GTGTGAGTTG AGTCTCCTCT CTGAGACTGC TAAGTAGGGG         1428
162 CAGTGATGGT TGCCAGGACG AATTGAGATA ATATCTGTGA GGTGCTGATG AGTGATTGAC         1488
164 ACACAGCACT CTCTAAATCT TCCTTGTGAG GATTATGGGT CCTGCAATTC TACAGTTTCT         1548
166 TACTGTTTTG TATCAAAATC ACTATCTTTC TGATAACAGA ATTGCCAAGG CAGCGGGATC         1608
168 TCGTATCTTT AAAAAGCAGT CCTCTTATTC CTAAGGTAAT CCTATTAAAA CACAGCTTTA         1668
170 CAACTTCCAT ATTACAAAAA AAAAAAAAAA AAA                                      1701
174 (2) INFORMATION FOR SEQ ID NO: 2:
176       (i) SEQUENCE CHARACTERISTICS:
177           (A) LENGTH: 256 amino acids
178           (B) TYPE: amino acid
179           (D) TOPOLOGY: linear
181       (ii) MOLECULE TYPE: protein
183       (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:
185 Val Asn Gln Ala Pro Glu Cys Arg Phe Gly Gly Gly Ile Leu Gly Pro
186   1               5                  10                  15
188 Leu Gly Lys Arg Arg Asp Leu Ala Arg Ala Ser Glu Pro Arg Thr Glu
189              20                  25                  30
191 Gly Ala Arg Arg Ala Gly Pro Gln Pro Arg Pro Leu Ala Asp Pro Ala
192              35                  40                  45
194 Met Asp Pro Phe Leu Val Leu Leu His Ser Val Ser Ser Ser Leu Ser
195      50                  55                  60
197 Ser Ser Glu Leu Thr Glu Leu Lys Phe Leu Cys Leu Gly Arg Val Val
198  65                  70                  75                  80
200 Lys Arg Lys Leu Glu Arg Val Gln Ser Gly Leu Asp Leu Phe Ser Met
201              85                  90                  95
203 Leu Leu Glu Gln Asn Asp Leu Glu Pro Gly His Thr Glu Leu Leu Arg
204             100                 105                 110
206 Glu Leu Leu Ala Ser Leu Arg Arg His Asp Leu Leu Arg Arg Val Asp
207             115                 120                 125
209 Asp Phe Glu Ala Gly Ala Ala Ala Gly Ala Ala Pro Gly Glu Glu Asp
210     130                 135                 140
212 Leu Cys Ala Ala Phe Asn Val Ile Cys Asp Asn Val Gly Lys Asp Trp
213 145                 150                 155                 160
215 Arg Arg Leu Ala Arg Gln Leu Lys Val Ser Asp Thr Lys Ile Asp Ser
216             165                 170                 175
218 Ile Glu Asp Arg Tyr Pro Arg Asn Leu Thr Glu Arg Val Arg Glu Ser
```

```
219              180                185                190
221 Leu Arg Ile Trp Lys Asn Thr Glu Lys Glu Asn Ala Thr Val Ala His
222         195                200                205
224 Leu Val Gly Ala Leu Arg Ser Cys Gln Met Asn Leu Val Ala Asp Leu
225     210                215                220
227 Val Gln Glu Val Gln Gln Ala Arg Asp Leu Gln Asn Arg Ser Gly Ala
228 225                230                235                240
230 Met Ser Pro Met Ser Trp Asn Ser Asp Ala Ser Thr Ser Glu Ala Ser
231             245                250                255
```

VERIFICATION SUMMARY
PATENT APPLICATION: US/09/824,134

DATE: 06/26/2001
TIME: 15:11:32

Input Set : N:\Crf3\RULE60\09824134.txt
Output Set: N:\CRF3\06262001\I824134.raw

L:31 M:220 C: Keyword misspelled or invalid format, [(A) APPLICATION NUMBER:]
L:32 M:220 C: Keyword misspelled or invalid format, [(B) FILING DATE:]